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Identification of Misregulated Proteins by Proteomics and Empathy of Biomarkers in Aggressive Ductal Carcinoma

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Abstract

Proteomics is the study of the entire protein complement of an organism, organ, tissue, or biological fluid. Proteomics-based identification of dysregulated proteins and biomarker discovery has become an essential tool for early detection, diagnosis, and treatment of various diseases, including cancer. Invasive ductal carcinoma (IDC) is the most common type of breast cancer, accounting for approximately 80% of all breast cancers. Proteomics-based approaches have been used to identify dysregulated proteins and biomarkers in IDC, which can potentially improve early detection, diagnosis, and treatment. MS is a technique that can be used to identify proteins based on their mass-to-charge ratio. Proteins are first digested into peptides using a protease such as trypsin. The resulting peptides are then ionized and introduced into the mass spectrometer. The mass spectrometer separates the peptides based on their mass-to-charge ratio and generates a mass spectrum. The mass spectrum can be used to identify the proteins present in the sample.MS can be used to identify dysregulated proteins in IDC by comparing the protein expression profiles of normal and cancerous tissues. Proteins that are overexpressed or under expressed in cancerous tissues can be identified using MS. These dysregulated proteins can then be validated using other proteomics techniques such as western blotting or immunohistochemistry.

Keywords: Carcinoma • Proteomics • Biomarkers

Introduction

Proteomics-based approaches such as two-dimensional gel electrophoresis (2DGE), liquid chromatography-mass spectrometry (LC-MS), and shotgun proteomics have been used to identify dysregulated proteins in IDC. 2DGE separates proteins based on their isoelectric point (pI) and molecular weight (MW). Differential expression of proteins is determined by comparing the intensity of spots on the gels. LC-MS identifies and quantifies proteins based on their mass-to-charge ratio (m/z) and provides more accurate protein identification than 2DGE. Shotgun proteomics uses high-throughput mass spectrometry to identify and quantify thousands of proteins simultaneously.

Several dysregulated proteins have been identified in IDC using these proteomics-based approaches. For example, the expression of alpha-enolase, a glycolytic enzyme, is upregulated in IDC and is associated with poor prognosis. Similarly, the expression of peroxiredoxin-1, a redox-regulating protein, is upregulated in IDC and is associated with tumor aggressiveness. Proteins such as heat shock protein 27 (HSP27) and glucose-regulated protein 78 (GRP78) have been found to be upregulated in IDC and are associated with chemoresistance. On the other hand, the expression of proteins such as annexin A1 and calreticulin is downregulated in IDC and is associated with tumor progression [1].

Literature Review

Biomarkers are biological molecules that can be used to detect the presence of a disease, monitor disease progression, or predict the response to therapy. Proteomics-based approaches have been used to discover biomarkers in IDC, which can potentially improve early detection, diagnosis, and treatment. One of the challenges in biomarker discovery is the identification of biomarkers that are specific to IDC and not expressed in normal breast tissue. Proteomics-based approaches such as LC-MS and shotgun proteomics have been used to identify proteins that are specifically expressed in IDC. For example, proteomic analysis of breast ductal fluid has identified several proteins that are specifically expressed in IDC, including S100A8, S100A9, and S100A11. These proteins have been proposed as potential biomarkers for early detection of IDC.

Another challenge in biomarker discovery is the validation of potential biomarkers in large cohorts of patients. Proteomics-based approaches such as selected reaction monitoring (SRM) and multiple reaction monitoring (MRM) have been used to validate potential biomarkers in large cohorts of patients. SRM and MRM are targeted proteomics approaches that use mass spectrometry to quantify specific peptides derived from the protein of interest. This allows for more accurate and precise quantification of potential biomarkers.

Discussion

Several potential biomarkers have been identified and validated in IDC using proteomics-based approaches. For example, the expression of cathepsin D, a lysosomal protease, is elevated in IDC and is associated with poor prognosis. The expression of protein tyrosine phosphatase receptor type C (PTPRC), also known as CD45, is elevated in IDC and is associated with tumor progression. The expression of insulin-like growth factor. Invasive ductal carcinoma (IDC) is the most common type of breast cancer, accounting for approximately 80% of all breast cancer cases. IDC is characterized by the proliferation of malignant epithelial cells in the ductal system of the breast. Despite advances in diagnosis and treatment, breast cancer remains a leading cause of cancer-related deaths worldwide. Early detection and diagnosis of IDC are essential for improving patient outcomes. Proteomics, the study of proteins and their functions, has emerged as a powerful tool for identifying dysregulated proteins and discovering biomarkers for IDC [2-4].

Proteomics has the potential to identify dysregulated proteins that play a role in the development and progression of IDC. Dysregulated proteins are proteins that are overexpressed or under expressed in cancer cells compared to normal cells. Proteomics techniques such as two-dimensional gel electrophoresis (2DGE) and mass spectrometry (MS) can be used to identify dysregulated

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proteins in IDC. 2DGE separates proteins based on their isoelectric point and molecular weight. This technique can be used to compare the protein expression profiles of normal and cancerous tissues. Dysregulated proteins can be identified as spots on the 2DGE gel that are differentially expressed between normal and cancerous tissues. These spots can then be excised from the gel and identified using MS [5,6].

While using salivary stress biomarkers like cortisol and alpha-amylase as a diagnostic tool is generally beneficial, it is far from perfect. They, for example, are unable to distinguish between acute fear and chronic anxiety. Furthermore, salivary cortisol levels reflect free serum cortisol levels, which are the unbound and biologically active 5% of total cortisol under basal conditions. Measurement of plasma cortisol concentration, on the other hand, yields total cortisol. In other words, salivary cortisol can only be used as a proxy for free serum cortisol levels. Another study found that assessing manganese exposure through saliva samples requires more research. Manganese exposure in water and salivary levels have the weakest correlation of the candidate biomarkers, including saliva, hair, and toes.

Conclusion

Biomarkers are measurable indicators of biological processes, disease processes, or responses to therapy. Biomarkers can be used for early detection, diagnosis, prognosis, and monitoring of disease. Proteomics has the potential to discover biomarkers for IDC. Biomarkers for IDC can be discovered using proteomics techniques such as MS-based proteomics, antibody-based proteomics, and aptamer-based proteomics. MS-based proteomics can be used to identify dysregulated proteins that can serve as biomarkers. Antibody-based proteomics uses antibodies to capture and identify proteins present in biological samples. Aptamer-based proteomics uses aptamers, which are short nucleic acid sequences that can bind to specific proteins, to capture and identify proteins present in biological samples. Several biomarkers for IDC have been discovered using proteomics. For example, the protein has been identified as a biomarker for IDC using MS-based proteomics. Proteomics has emerged as a powerful tool for identifying dysregulated proteins and discovering biomarkers for IDC. Dysregulated proteins can be identified using proteomics techniques such as 2DGE and MS. Biomarkers for IDC can be discovered using proteomics techniques such as MS-based proteomics, antibody-based proteomics, and aptamer-based proteomics

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Conflict of Interest

There are no conflicts of interest by author.

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